SEQUENCE LISTING

<110> Conklin, Darrell C.
      Yamamoto, Gayle
      Gao, Zeren
      Jaspers, Stephen

<120> BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOG,
  ZNSSP6

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<151> 1999-01-12

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<210> 1
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<213> Homo sapiens

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<222> (135)...(1271)

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actcatctcg cttcgacccc gccgccgccg ccgcccggca tcctgagcac ggagacagtc   120
tccagctgcc gttc atg ctt cct ccc cag cct tcc gca gcc cac cag gga   170
              Met Leu Pro Pro Gln Pro Ser Ala Ala His Gln Gly
               1   5   10

agg ggc ggt agg agt ggc ctt tta cca aag gga ccg gcg atg ctc tgc   218
Arg Gly Gly Arg Ser Gly Leu Leu Pro Lys Gly Pro Ala Met Leu Cys
       15   20   25

agg ctg tgc tgg ctg gtc tcg tac agc ttg gct gtg ctg ttg ctc ggc   266
Arg Leu Cys Trp Leu Val Ser Tyr Ser Leu Ala Val Leu Leu Leu Gly
      30   35   40

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tgc ctg ctc ttc ctg agg aag gcg gcc aag ccc gca gga gac ccc acg        314
Cys Leu Leu Phe Leu Arg Lys Ala Ala Lys Pro Ala Gly Asp Pro Thr
 45                  50                  55                  60

gcc cac cag cct ttc tgg gct ccc cca aca ccc cgt cac agc cgg tgt        362
Ala His Gln Pro Phe Trp Ala Pro Pro Thr Pro Arg His Ser Arg Cys
                65                  70                  75

cca ccc aac cac aca gtg tct agc gcc tct ctg tcc ctg cct agc cgt        410
Pro Pro Asn His Thr Val Ser Ser Ala Ser Leu Ser Leu Pro Ser Arg
                80                  85                  90

cac cgt ctc ttc ttg acc tat cgt cac tgc cga aat ttc tct atc ttg        458
His Arg Leu Phe Leu Thr Tyr Arg His Cys Arg Asn Phe Ser Ile Leu
                95                 100                 105

ctg gag cct tca ggc tgt tcc aag gat acc ttc ttg ctc ctg gcc atc        506
Leu Glu Pro Ser Gly Cys Ser Lys Asp Thr Phe Leu Leu Leu Ala Ile
        110                 115                 120

aag tca cag cct ggt cac gtg gag cga cgt gcg gct atc cgc agc acg        554
Lys Ser Gln Pro Gly His Val Glu Arg Arg Ala Ala Ile Arg Ser Thr
125                 130                 135                 140

tgg ggc agg gtg ggg gga tgg gct agg ggc cgg cag ctg aag ctg gtg        602
Trp Gly Arg Val Gly Gly Trp Ala Arg Gly Arg Gln Leu Lys Leu Val
                145                 150                 155

ttc ctc cta ggg gtg gca gga tcc gct ccc cca gcc cag ctg ctg gcc        650
Phe Leu Leu Gly Val Ala Gly Ser Ala Pro Pro Ala Gln Leu Leu Ala
                160                 165                 170

tat gag agt agg gag ttt gat gac atc ctc cag tgg gac ttc act gag        698
Tyr Glu Ser Arg Glu Phe Asp Asp Ile Leu Gln Trp Asp Phe Thr Glu
                175                 180                 185

gac ttc ttc aac ctg acg ctc aag gag ctg cac ctg cag cgc tgg gtg        746
Asp Phe Phe Asn Leu Thr Leu Lys Glu Leu His Leu Gln Arg Trp Val
        190                 195                 200

gtg gct gcc tgc ccc cag gcc cat ttc atg cta aag gga gat gac gat        794
Val Ala Ala Cys Pro Gln Ala His Phe Met Leu Lys Gly Asp Asp Asp
205                 210                 215                 220
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gtc ttt gtc cac gtc ccc aac gtg tta gag ttc ctg gat ggc tgg gac      842
Val Phe Val His Val Pro Asn Val Leu Glu Phe Leu Asp Gly Trp Asp
            225              230              235

cca gcc cag gac ctc ctg gtg gga gat gtc atc cgc caa gcc ctg ccc      890
Pro Ala Gln Asp Leu Leu Val Gly Asp Val Ile Arg Gln Ala Leu Pro
            240              245              250

aac agg aac act aag gtc aaa tac ttc atc cca ccc tca atg tac agg      938
Asn Arg Asn Thr Lys Val Lys Tyr Phe Ile Pro Pro Ser Met Tyr Arg
            255              260              265

gcc acc cac tac cca ccc tat gct ggt ggg gga gga tat gtc atg tcc      986
Ala Thr His Tyr Pro Pro Tyr Ala Gly Gly Gly Gly Tyr Val Met Ser
            270              275              280

aga gcc aca gtg cgg cgc ctc cag gct atc atg gaa gat gct gaa ctc     1034
Arg Ala Thr Val Arg Arg Leu Gln Ala Ile Met Glu Asp Ala Glu Leu
285              290              295              300

ctc tcc att gat gat gtc ttt gtg ggt atg tgc ctg agg agg ctg ggg     1082
Leu Ser Ile Asp Asp Val Phe Val Gly Met Cys Leu Arg Arg Leu Gly
            305              310              315

ctg agc cct atg cac cat gct ggc ttc aag aca ttt gga atc cgg cgg     1130
Leu Ser Pro Met His His Ala Gly Phe Lys Thr Phe Gly Ile Arg Arg
            320              325              330

ccc ctg gac ccc tta gac ccc tgc ctg tat agg ggg ctc ctg ctg gtt     1178
Pro Leu Asp Pro Leu Asp Pro Cys Leu Tyr Arg Gly Leu Leu Leu Val
            335              340              345

cac cgc ctc agc ccc ctc gag atg tgg acc atg tgg gca ctg gtg aca     1226
His Arg Leu Ser Pro Leu Glu Met Trp Thr Met Trp Ala Leu Val Thr
            350              355              360

gat gag ggg ctc aag tgt gca gct ggc ccc ata ccc cag cgc tga        1271
Asp Glu Gly Leu Lys Cys Ala Ala Gly Pro Ile Pro Gln Arg *
365              370              375
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agggtgggtt gggcaacagc ctgagagtgg actcagtgtt gattctctat cgtgatgcga    1331
aattgatgcc tgctgctcta cagaaaatgc caacttggtt ttttaactcc tctcaccctg    1391
ttagctctga ttaaaaacac tgcaaccca                                      1420
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Ser Gly Leu Leu Pro Lys Gly Pro Ala Met Leu Cys Arg Leu Cys Trp
            20              25                  30
Leu Val Ser Tyr Ser Leu Ala Val Leu Leu Leu Gly Cys Leu Leu Phe
            35              40                  45
Leu Arg Lys Ala Ala Lys Pro Ala Gly Asp Pro Thr Ala His Gln Pro
        50              55                  60
Phe Trp Ala Pro Pro Thr Pro Arg His Ser Arg Cys Pro Pro Asn His
65                  70                  75                  80
Thr Val Ser Ser Ala Ser Leu Ser Leu Pro Ser Arg His Arg Leu Phe
                85                  90                  95
Leu Thr Tyr Arg His Cys Arg Asn Phe Ser Ile Leu Leu Glu Pro Ser
            100                 105                 110
Gly Cys Ser Lys Asp Thr Phe Leu Leu Leu Ala Ile Lys Ser Gln Pro
            115                 120                 125
Gly His Val Glu Arg Arg Ala Ala Ile Arg Ser Thr Trp Gly Arg Val
            130                 135                 140
Gly Gly Trp Ala Arg Gly Arg Gln Leu Lys Leu Val Phe Leu Leu Gly
145                 150                 155                 160
Val Ala Gly Ser Ala Pro Pro Ala Gln Leu Leu Ala Tyr Glu Ser Arg
                165                 170                 175
Glu Phe Asp Asp Ile Leu Gln Trp Asp Phe Thr Glu Asp Phe Phe Asn
                180                 185                 190
Leu Thr Leu Lys Glu Leu His Leu Gln Arg Trp Val Val Ala Ala Cys
            195                 200                 205
Pro Gln Ala His Phe Met Leu Lys Gly Asp Asp Asp Val Phe Val His
    210                 215                 220
Val Pro Asn Val Leu Glu Phe Leu Asp Gly Trp Asp Pro Ala Gln Asp
225                 230                 235                 240
Leu Leu Val Gly Asp Val Ile Arg Gln Ala Leu Pro Asn Arg Asn Thr
                245                 250                 255
Lys Val Lys Tyr Phe Ile Pro Pro Ser Met Tyr Arg Ala Thr His Tyr
                260                 265                 270
Pro Pro Tyr Ala Gly Gly Gly Gly Tyr Val Met Ser Arg Ala Thr Val
            275                 280                 285
Arg Arg Leu Gln Ala Ile Met Glu Asp Ala Glu Leu Leu Ser Ile Asp
    290                 295                 300
Asp Val Phe Val Gly Met Cys Leu Arg Arg Leu Gly Leu Ser Pro Met
305                 310                 315                 320
```

```
 His His Ala Gly Phe Lys Thr Phe Gly Ile Arg Arg Pro Leu Asp Pro
                 325                 330                 335
 Leu Asp Pro Cys Leu Tyr Arg Gly Leu Leu Leu Val His Arg Leu Ser
                 340                 345                 350
 Pro Leu Glu Met Trp Thr Met Trp Ala Leu Val Thr Asp Glu Gly Leu
                 355                 360                 365
 Lys Cys Ala Ala Gly Pro Ile Pro Gln Arg
                 370                 375
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        <210> 3
        <211> 1134
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> degenerate sequence

        <221> variation
        <222> (1)...(1134)
        <223> n is any nucleotide

        <221> misc_feature
        <222> (1)...(1134)
        <223> n = A,T,C or G

        <400> 3
  atgytnccnc cncarccnws ngcngcncay carggnmgng gnggnmgnws nggnytnytn      60
  ccnaarggnc cngcnatgyt ntgymgnytn tgytggytng tnwsntayws nytngcngtn     120
  ytnytnytng gntgyytnyt nttyytnmgn aargcngcna arccngcngg ngayccnacn     180
  gcncaycarc cnttytgggc nccnccnacn ccnmgncayw snmgntgycc nccnaaycay     240
  acngtnwsnw sngcnwsnyt nwsnytnccn wsnmgncaym gnytnttyyt nacntaymgn     300
  caytgymgna ayttywsnat hytnytngar ccnwsnggnt gywsnaarga yacnttyytn     360
  ytnytngcna thaarwsnca rccnggncay gtngarmgnm gngcngcnat hmgnwsnacn     420
  tggggnmgng tnggnggntg ggcnmgnggn mgncarytna arytngtntt yytnytnggn     480
  gtngcnggnw sngcnccncc ngcncaaryt nytngcntayg arwsnmgnga rttygaygay     540
  athytncart gggayttyac ngargaytty ttyaayytna cnytnaarga rytncayytn     600
  carmgntggg tngtngcngc ntgyccncar gcncayttya tgytnaargg ngaygaygay     660
  gtnttygtnc aygtnccnaa ygtnytngar ttyytngayg gntgggaycc ngcncargay     720
  ytnytngtng gngaygtnat hmgncargcn ytnccnaaym gnaayacnaa rgtnaartay     780
  ttyathccnc cnwsnatgta ymgngcnacn caytayccnc cntaygcngg nggnggnggn     840
  taygtnatgw snmgngcnac ngtnmgnmgn ytncargcna thatggarga ygcngarytn     900
  ytnwsnathg aygaygtntt ygtnggnatg tgyytnmgnm gnytnggnyt nwsnccnatg     960
  caycaygcng gnttyaarac nttyggnath mgnmgnccny tngayccnyt ngayccntgy    1020
  ytntaymgng gnytnytnyt ngtncaymgn ytnwsnccny tngaratgtg gacnatgtgg    1080
  gcnytngtna cngaygargg nytnaartgy gcngcnggnc cnathccnca rmgn          1134
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<210> 4
<211> 27
<212> DNA
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<220>
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<400> 4
ccatcctaat acgactcact atagggc   27

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 5
cggatagccg cacgtcgctc cac   23

<210> 6
<211> 23
<212> DNA
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<220>
<223> oligonucleotide primer

<400> 6
actcactata gggctcgagc ggc   23

<210> 7
<211> 23
<212> DNA
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<220>
<223> oligonucleotide primer

<400> 7
tgaccaggct gtgacttgat ggc   23

<210> 8
<211> 24
<212> DNA
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<220>
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<400> 8
cttggcacga ggcacgagct ccac   24

<210> 9
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<400> 9
ctcaggctgt tgcccaaccc accc   24

<210> 10
<211> 25
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<400> 10
gtcttgaagc cagcatggtg catag   25

<210> 11
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<400> 11
gggagtttga tgacatcctc cagtg   25

<210> 12

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<220>
<223> oligonucleotide primer

<400> 12
gccaagcccg caggagac   18

<210> 13
<211> 18
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<220>
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<400> 13
acggctaggc agggacag   18

<210> 14
<211> 66
<212> DNA
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<220>
<223> Oligonucleotide primer

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aaattataaa aatatccaaa cacgcagccc tagaatacta gtcatctctg gggtatgggg   60
ccagct   66

<210> 15
<211> 65
<212> DNA
<213> OlArtificial Sequence

<220>
<223> Oligonucleotide primer

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ggacaagaga gaagaagaat acatgccaat ggaaggtggt aggaaggctg ccaaacccgc   60
aggag   65

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<210> 16
<211> 65
<212> DNA
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<220>
<223> Oligonucleotide primer

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aggag                                                                65


<210> 17
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 17
actaggaatt ctactccata ggcatatact cctcgcctcc gcgttggggt atggggccag    60
ctgca                                                                65


<210> 18
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 18
cattgctgct aaagaagaag gtgtaagctt ggacaagaga aggaaggcgg ctaagcccgc    60
aggag                                                                65


<210> 19
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 19
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catagtttct ttcttaacag atatgggcag aagaaatggc tgaatgcctc tggccatagc      60
ggccggcccc taggatccga attctagaag ctttgtgtct caaaatctct gatgttacat     120
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